



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/840 669  
Source: O I P E  
Date Processed by STIC: 08/27/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/840,669

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11    Use of <220>  
Sequence(s)    missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The type of errors shown <sup>may</sup> exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIFE

## RAW SEQUENCE LISTING

DATE: 08/27/2001

PATENT APPLICATION: US/09/840,669

TIME: 15:10:37

Input Set : A:\A-690.ST25.txt

Output Set: N:\CRF3\08272001\I840669.raw

3 <110> APPLICANT: KOHNO, TADAHIKO  
5 <120> TITLE OF INVENTION: APO-AI/AII PEPTIDE DERIVATIVES  
7 <130> FILE REFERENCE: A-690  
9 <140> CURRENT APPLICATION NUMBER: 09/840,669  
10 <141> CURRENT FILING DATE: 2001-04-23  
12 <150> PRIOR APPLICATION NUMBER: 60/198,920  
13 <151> PRIOR FILING DATE: 2000-04-21  
15 <160> NUMBER OF SEQ ID NOS: 11  
17 <170> SOFTWARE: PatentIn version 3.1  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 684  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Homo sapiens  
24 <220> FEATURE:  
25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (1)..(684)  
27 <223> OTHER INFORMATION:  
30 <400> SEQUENCE: 1

31	atg	gac	aaa	act	cac	aca	tgt	cca	cct	tgt	cca	gct	ccg	gaa	ctc	ctg	48
32	Met	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
33	1			5						10				15			
35	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	96
36	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
37				20					25					30			
39	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	144
40	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
41				35					40					45			
43	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	192
44	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
45		50					55					60					
47	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	240
48	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	
49	65					70				75				80			
51	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	288
52	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	
53				85					90					95			
55	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	336
56	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	
57				100					105					110			
59	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	384
60	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	
61			115				120					125					
63	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	432
64	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	
65			130				135					140					
67	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	480
68	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	

Does Not Comply  
Corrected Diskette Needed  
See page 3 of 7

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DATE: 08/27/2001

PATENT APPLICATION: US/09/840,669

TIME: 15:10:37

Input Set : A:\A-690.ST25.txt

Output Set: N:\CRF3\08272001\I840669.raw

```

69 145          150          155          160
71 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
72 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
73          165          170          175
75 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
76 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
77          180          185          190
79 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
80 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
81          195          200          205
83 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
84 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
85          210          215          220
87 tct ccg ggt aaa      684
88 Ser Pro Gly Lys
89 225
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 228
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 2
99 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
100 1          5          10          15
103 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
104          20          25          30
107 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
108          35          40          45
111 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
112          50          55          60
115 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
116 65          70          75          80
119 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
120          85          90          95
123 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
124          100          105          110
127 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
128          115          120          125
131 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
132          130          135          140
135 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
136 145          150          155          160
139 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
140          165          170          175
143 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
144          180          185          190
147 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
148          195          200          205
151 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
152          210          215          220

```

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DATE: 08/27/2001

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Input Set : A:\A-690.ST25.txt

Output Set: N:\CRF3\08272001\I840669.raw

155 Ser Pro Gly Lys  
 156 225  
 159 <210> SEQ ID NO: 3  
 160 <211> LENGTH: 8  
 161 <212> TYPE: PRT  
 162 <213> ORGANISM: Artificial Sequence  
 164 <220> FEATURE:  
 165 <223> OTHER INFORMATION: Preferred linker *OK*  
 167 <400> SEQUENCE: 3  
 169 Gly Gly Gly Lys Gly Gly Gly  
 170 1 5  
 173 <210> SEQ ID NO: 4  
 174 <211> LENGTH: 7  
 175 <212> TYPE: PRT  
 176 <213> ORGANISM: Artificial Sequence  
 178 <220> FEATURE:  
 179 <223> OTHER INFORMATION: Preferred linker *OK*  
 181 <400> SEQUENCE: 4  
 183 Gly Gly Asn Gly Ser Gly Gly  
 184 1 5  
 187 <210> SEQ ID NO: 5  
 188 <211> LENGTH: 8  
 189 <212> TYPE: PRT  
 190 <213> ORGANISM: Artificial Sequence  
 192 <220> FEATURE:  
 193 <223> OTHER INFORMATION: Preferred linker *OK*  
 195 <400> SEQUENCE: 5  
 197 Gly Gly Gly Cys Gly Gly Gly  
 198 1 5  
 201 <210> SEQ ID NO: 6  
 202 <211> LENGTH: 5  
 203 <212> TYPE: PRT  
 204 <213> ORGANISM: Artificial Sequence  
 206 <220> FEATURE:  
 207 <223> OTHER INFORMATION: Preferred linker ✓  
 209 <400> SEQUENCE: 6  
 211 Gly Pro Asn Gly Gly  
 212 1 5  
 215 <210> SEQ ID NO: 7  
 216 <211> LENGTH: 18  
 217 <212> TYPE: PRT  
 218 <213> ORGANISM: Artificial Sequence  
 220 <220> FEATURE:  
 221 <223> OTHER INFORMATION: Peptide *Errored*  
 223 <400> SEQUENCE: 7  
 225 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
 226 1 5 10 15  
 229 Ala Phe  
 233 <210> SEQ ID NO: 8

The 213 response Artificial  
 Sequence requires an explanation  
 in field 223. Peptide is not  
 a sufficient description

*may*  
 The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

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DATE: 08/27/2001  
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Input Set : A:\A-690.ST25.txt  
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234 <211> LENGTH: 18  
235 <212> TYPE: PRT  
236 <213> ORGANISM: Artificial Sequence ✓  
238 <220> FEATURE:  
239 <223> OTHER INFORMATION: Preferred embodiments ✓  
241 <220> FEATURE:  
242 <221> NAME/KEY: misc\_feature  
243 <222> LOCATION: (18)..(18)  
244 <223> OTHER INFORMATION: Fc domain attached at Position 18 through an optional linker  
247 <400> SEQUENCE: 8  
249 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
250 1 5 10 15  
253 Ala Phe  
257 <210> SEQ ID NO: 9  
258 <211> LENGTH: 18  
259 <212> TYPE: PRT  
260 <213> ORGANISM: Artificial Sequence  
262 <220> FEATURE:  
263 <223> OTHER INFORMATION: Preferred embodiments OK  
265 <220> FEATURE:  
266 <221> NAME/KEY: misc\_feature  
267 <222> LOCATION: (1)..(1)  
268 <223> OTHER INFORMATION: Fc domain attached through optional linker  
271 <400> SEQUENCE: 9  
273 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
274 1 5 10 15  
277 Ala Phe  
281 <210> SEQ ID NO: 10  
282 <211> LENGTH: 18  
283 <212> TYPE: PRT  
284 <213> ORGANISM: Artificial Sequence  
286 <220> FEATURE:  
287 <223> OTHER INFORMATION: Preferred embodiments  
289 <220> FEATURE:  
290 <221> NAME/KEY: misc\_feature  
291 <222> LOCATION: (19)..(19)  
292 <223> OTHER INFORMATION: Attached by optional linker to identical sequence, which is  
attac hed by optional linker to an Fc domain  
293  
296 <400> SEQUENCE: 10  
298 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
299 1 5 10 15  
302 Ala Phe  
306 <210> SEQ ID NO: 11  
307 <211> LENGTH: 18  
308 <212> TYPE: PRT  
309 <213> ORGANISM: Artificial Sequence  
311 <220> FEATURE:  
312 <223> OTHER INFORMATION: Preferred embodiments  
314 <220> FEATURE:

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Input Set : A:\A-690.ST25.txt

Output Set: N:\CRF3\08272001\I840669.raw

315 <221> NAME/KEY: misc\_feature  
316 <222> LOCATION: (1)..(1)  
317 <223> OTHER INFORMATION: Attached by optional linker to Fc domain at the N-terminus.  
321 <220> FEATURE:  
322 <221> NAME/KEY: misc\_feature  
323 <222> LOCATION: (18)..(18)  
324 <223> OTHER INFORMATION: Attached by optional linker to an identical sequence  
327 <400> SEQUENCE: 11  
329 Asp Trp Leu Lys Ala Phe Tyr Asp Lys Val Ala Glu Lys Leu Lys Glu  
330 1                   5                   10                   15  
333 Ala Phe

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/840,669

DATE: 08/27/2001

TIME: 15:10:38

Input Set : A:\A-690.ST25.txt

Output Set: N:\CRF3\08272001\I840669.raw